

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=7; day=7; hr=13; min=47; sec=16; ms=579;]

=====

Application No: 10582304

Version No: 2.0

Input Set:

Output Set:

Started: 2009-07-06 12:46:32.719

Finished: 2009-07-06 12:46:34.629

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 910 ms

Total Warnings: 15

Total Errors: 0

No. of SeqIDs Defined: 29

Actual SeqID Count: 29

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)

SEQUENCE LISTING

<110> KIMURA, NAOKI
TSUCHIYA, MASAYUKI
NANAMI, MASAHIKO
TOMIMATSU, TAKASHI
KAWAI, SHIGETO

<120> Cell Death Inducing Agent

<130> 14875-0166US1

<140> 10582304

<141> 2009-07-06

<150> PCT/JP2004/018501

<151> 2004-12-10

<150> JP 2003-415758

<151> 2003-12-12

<160> 29

<170> PatentIn version 3.1

<210> 1

<211> 1572

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (14)..(1561)

<400> 1

cctgaattcc acc atg cga tgg agc tgg atc ttt ctc ttc ctc ctg tca	49
Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser	
1 5 10	

ata act gca ggt gtc cat tgc cag gtc cag ttg cag cag tct gga cct	97
Ile Thr Ala Gly Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro	
15 20 25	

gag ctg gtg aag cct ggg gct tca gtg aag atg tct tgt aag gct tct	145
Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser	
30 35 40	

ggc tac acc ttc aca gac tac ttt ata cac tgg gtg aaa cag agg cct	193
Gly Tyr Thr Phe Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro	
45 50 55 60	

gga cag gga ctt gaa tgg att gga tgg att ttt cct gga gat gat act	241
Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr	
65 70 75	

act gat tac aat gag aag ttc agg ggc aag acc aca ctg act gca gac	289
-----------------------------------------------------------------	-----

Thr Asp Tyr Asn Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp	
80	85
90	
aaa tcc tcc agc aca gcc tac att ttg ctc agc agc ctg acc tct gag	337
Lys Ser Ser Ser Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu	
95	100
105	
gac tct gcg atg tat ttc tgt gta agg agt gac gac ttt gac tac tgg	385
Asp Ser Ala Met Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp	
110	115
120	
ggc cag ggc acc act ctc aca gtc tcc tca ggt gga ggc ggt tca ggc	433
Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
125	130
135	140
gga ggt ggc tct ggc ggt ggc gga agc caa att gtt ctc acc cag tcg	481
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser	
145	150
155	
cca gca atc atg tct gca tct cca ggg gag aag gtc acc ata acc tgc	529
Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys	
160	165
170	
agt gcc agc tca agt gta agt tac atg cac tgg ttc cag cag aag cca	577
Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro	
175	180
185	
ggc act ttt ccc aaa ctc tgg att tat agc aca tcc aac ctg gct tct	625
Gly Thr Phe Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser	
190	195
200	
gga gtc cct act cgc ttc agt ggc agt gga tct ggg acc tct tac tct	673
Gly Val Pro Thr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser	
205	210
215	220
ctc aca atc agc cga atg gag gct gaa gat gct gcc act tat tac tgc	721
Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys	
225	230
235	
cag caa agg acg agt tat cca ccc acg ttc ggc tcg ggg aca aag ttg	769
Gln Gln Arg Thr Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu	
240	245
250	
gag ata aaa gga ggt ggt ggc agt ggt ggc ggc gga tcc ggt ggc ggt	817
Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly	
255	260
265	
ggc tca cag gtc cag ttg cag cag tct gga cct gag ctg gtg aag cct	865
Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro	
270	275
280	
ggg gct tca gtg aag atg tct tgt aag gct tct ggc tac acc ttc aca	913
Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr	
285	290
295	300
gac tac ttt ata cac tgg gtg aaa cag agg cct gga cag gga ctt gaa	961
Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu	

305	310	315	
tgg att gga tgg att ttt cct gga gat gat act act gat tac aat gag			1009
Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn Glu			
320	325	330	
aag ttc agg ggc aag acc aca ctg act gca gac aaa tcc tcc agc aca			1057
Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr			
335	340	345	
gcc tac att ttg ctc agc agc ctg acc tct gag gac tct gcg atg tat			1105
Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met Tyr			
350	355	360	
ttc tgt gta agg agt gac gac ttt gac tac tgg ggc cag ggc acc act			1153
Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr			
365	370	375	380
ctc aca gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc			1201
Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly			
385	390	395	
ggg ggc gga agc caa att gtt ctc acc cag tcg cca gca atc atg tct			1249
Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser			
400	405	410	
gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc tca agt			1297
Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser			
415	420	425	
gta agt tac atg cac tgg ttc cag cag aag cca ggc act ttt ccc aaa			1345
Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro Lys			
430	435	440	
ctc tgg att tat agc aca tcc aac ctg gct tct gga gtc cct act cgc			1393
Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr Arg			
445	450	455	460
ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc agc cga			1441
Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg			
465	470	475	
atg gag gct gaa gat gct gcc act tat tac tgc cag caa agg acg agt			1489
Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr Ser			
480	485	490	
tat cca ccc acg ttc ggc tcg ggg aca aag ttg gag ata aaa gac tac			1537
Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Asp Tyr			
495	500	505	
aag gat gac gac gat aag tga taa gcggccgcaa t			1572
Lys Asp Asp Asp Asp Lys			
510			

<210> 2

<211> 514

<212> PRT

<213> Mus musculus

<400> 2

Met	Arg	Trp	Ser	Trp	Ile	Phe	Leu	Phe	Leu	Leu	Ser	Ile	Thr	Ala	Gly	
1				5					10					15		
Val	His	Cys	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	
			20					25					30			
Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
		35					40					45				
Thr	Asp	Tyr	Phe	Ile	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	
	50					55				60						
Glu	Trp	Ile	Gly	Trp	Ile	Phe	Pro	Gly	Asp	Asp	Thr	Thr	Asp	Tyr	Asn	
65					70				75						80	
Glu	Lys	Phe	Arg	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	
				85					90					95		
Thr	Ala	Tyr	Ile	Leu	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Met	
		100						105					110			
Tyr	Phe	Cys	Val	Arg	Ser	Asp	Asp	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	
		115					120					125				
Thr	Leu	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	
	130					135					140					
Gly	Gly	Gly	Gly	Ser	Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	
145					150					155					160	
Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	
				165					170					175		
Ser	Val	Ser	Tyr	Met	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Thr	Phe	Pro	
			180					185					190			
Lys	Leu	Trp	Ile	Tyr	Ser	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Thr	
		195					200					205				
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	
	210					215					220					
Arg	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Thr	
225					230					235					240	
Ser	Tyr	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	
				245					250					255		
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	
			260					265						270		
Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	Val	
		275					280						285			

Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Phe Ile
290 295 300

His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Trp
305 310 315 320

Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn Glu Lys Phe Arg Gly
325 330 335

Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Ile Leu
340 345 350

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met Tyr Phe Cys Val Arg
355 360 365

Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
370 375 380

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
385 390 395 400

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
405 410 415

Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
420 425 430

His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro Lys Leu Trp Ile Tyr
435 440 445

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr Arg Phe Ser Gly Ser
450 455 460

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
465 470 475 480

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr Ser Tyr Pro Pro Thr
485 490 495

Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp
500 505 510

Asp Lys

<210> 3

<211> 5

<212> PRT

<213> Mus musculus

<400> 3

Asp Tyr Phe Ile His

1 5

<210> 4
<211> 17
<212> PRT
<213> Mus musculus

<400> 4
Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn Glu Lys Phe Arg
1 5 10 15

Gly

<210> 5
<211> 6
<212> PRT
<213> Mus musculus

<400> 5
Ser Asp Asp Phe Asp Tyr
1 5

<210> 6
<211> 10
<212> PRT
<213> Mus musculus

<400> 6
Ser Ala Ser Ser Ser Val Ser Tyr Met His
1 5 10

<210> 7
<211> 7
<212> PRT
<213> Mus musculus

<400> 7
Ser Thr Ser Asn Leu Ala Ser
1 5

<210> 8
<211> 9
<212> PRT
<213> Mus musculus

<400> 8
Gln Gln Arg Thr Ser Tyr Pro Pro Thr
1 5

<210> 9
<211> 402
<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(402)

<400> 9

atg cga tgg agc tgg atc ttt ctc ttc ctc ctg tca ata act gca ggt 48

Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly

1 5 10 15

gtc cat tgc cag gtc cag ttg cag cag tct gga cct gag ctg gtg aag 96

Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys

20 25 30

cct ggg gct tca gtg aag atg tct tgt aag gct tct ggc tac acc ttc 144

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe

35 40 45

aca gac tac ttt ata cac tgg gtg aaa cag agg cct gga cag gga ctt 192

Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu

50 55 60

gaa tgg att gga tgg att ttt cct gga gat gat act act gat tac aat 240

Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn

65 70 75 80

gag aag ttc agg ggc aag acc aca ctg act gca gac aaa tcc tcc agc 288

Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser

85 90 95

aca gcc tac att ttg ctc agc agc ctg acc tct gag gac tct gcg atg 336

Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met

100 105 110

tat ttc tgt gta agg agt gac gac ttt gac tac tgg ggc cag ggc acc 384

Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr

115 120 125

act ctc aca gtc tcc tca 402

Thr Leu Thr Val Ser Ser

130

<210> 10

<211> 134

<212> PRT

<213> Mus musculus

<400> 10

Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly

1 5 10 15

Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys

20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe

35

40

45

Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn
 65 70 75 80

Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met
 100 105 110

Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr
 115 120 125

Thr Leu Thr Val Ser Ser
 130

<210> 11

<211> 384

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(384)

<400> 11

atg cat ttt caa gtg cag att ttc agc ttc ctg cta atc agt gcc tca 48
 Met His Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

gtc atc atg tcc aga gga caa att gtt ctc acc cag tcg cca gca atc 96
 Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
 20 25 30

atg tct gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc 144
 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser
 35 40 45

tca agt gta agt tac atg cac tgg ttc cag cag aag cca ggc act ttt 192
 Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe
 50 55 60

ccc aaa ctc tgg att tat agc aca tcc aac ctg gct tct gga gtc cct 240
 Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80

act cgc ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc 288
 Thr Arg Phe Ser Gly